

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Burkly, Linda C
Benjamin, Christopher D
Hession, Catherine A
Whitty, Adrian

(ii) TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Biogen, Inc.
(B) STREET: 14 Cambridge Center
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02142

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: A006 PCT CIP
(B) FILING DATE: 09-MAY-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/017,466
(B) FILING DATE: 10-MAY-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kaplan, Warren A.
(B) REGISTRATION NUMBER: 34,199
(C) REFERENCE/DOCKET NUMBER: A006 PCT CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: pLB001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGAAGC CATCATTACC ATTACATCC CTCTTATTCC TGCAGCTGCC CCTGCTGGGA 60
 GTGGGGCTGA ACACGACAAT TCTGACGCC AATGGGAATG AAGACACCAC AGCTGATTTT 120
 TTCCTGACCA CTATGCCCAC TGACTCCCTC AGTGTPTTCCA CTCTGCCCCCT CCCAGAGGTT 180
 CAGTGTPTTG TGTTCATGT CGAGTACATG AATTGCACTT GGAACAGCAG CTCTGAGCCC 240
 CAGCCTACCA ACCTCACTCT GCATTATTGG TACAAGAACT CGGATAATGA TAAAGTCCAG 300
 AAGTGCAGCC ACTATCTATT CTCTGAAGAA ATCACTTCTG GCTGTCAGTT GCAAAAAAAG 360
 GAGATCCACC TCTACCAAAC ATTTGTTGTT CAGCTCCAGG ACCCACGGGA ACCCAGGAGA 420
 CAGGCCACAC AGATGCTAAA ACTGCAGAA CTGGTGATCC CCTGGGCTCC AGAGAACCTA 480
 ACACTTCACA AACTGAGTGA ATCCCAGCTA GAACTGAACT GGAACAACAG ATTCTTGAAC 540
 CACTGTTTGG AGCACTTGGT GCAGTACCGG ACTGACTGGG ACCACAGCTG GACTGAACAA 600
 TCAGTGGATT ATAGACATAA GTTCTCCTTG CCTAGTGTGG ATGGGCAGAA ACGCTACATG 660
 TTTCGTGTTT GGAGCCGCTT TAACCCACTC TGTGGAAGTG CTCAGCATTG GAGTGAATGG 720
 AGCCACCCAA TCCACTGGGG GAGCAATACT TCAAAAGAGA ATGTCGACAA AACTCACACA 780
 TGCCACCGT GCCCAGCAC TGAACTCCTG GGGGACCGT CAGTCTTCCT CTTCCTCCCA 840
 AAACCCAAGG ACACCCTCAT GATCTCCCGG ACCCCTGAGG TCACATGCGT GGTGGTGGAC 900
 GTGAGCCACG AAGACCCTGA GGTCAAGTTC AACTGGTACG TGGACGGCGT GGAGGTGCAT 960
 AATGCCAAGA CAAAGCCGCG GGAGGAGCAG TACAACAGCA CGTACCGTGT GGTGAGCGTC 1020
 CTCACCGTCC TGCACCAGGA CTGGCTGAAT GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC 1080
 AAAGCCCTCC CAGCCCCCAT CGAGAAAACC ATCTCCAAAG CCAAGGGCA GCCCCGAGAA 1140
 CCACAGGTGT ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTGAGCCTG 1200
 ACCTGCCTGG TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG 1260
 CAGCCGGAGA ACAACTACAA GACCACGCCT CCGTGTGTTG ACTCCGACGG CTCCTTCTTC 1320
 CTCTACAGCA AGCTCACCCT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC 1380
 TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG 1440
 GGTAAG 1446

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
1          5          10          15
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
20          25          30
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
35          40          45
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
50          55          60
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65          70          75
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
85          90          95
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
100         105         110
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
115         120         125
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
130         135         140
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145         150         155         160
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
165         170         175
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
180         185         190
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
195         200         205
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Met Phe Arg Val Arg
210         215         220
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225         230         235         240
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Val Asp
245         250         255
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
260         265         270
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275         280         285
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290         295         300
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305         310         315         320

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Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 1 5 10 15
 Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
 20 25 30
 Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
 35 40 45
 Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu
 50 55 60
 Asn Ile Asn Arg Asp Asn Ser Lys Ser Gln Ile Phe Leu Lys Met Asn
 65 70 75 80

- 81 -

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Glu Gly
 85 90 95

Ser Thr Val Asp Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 100 105 110

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

Asp Ser Ile Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Thr Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ile Thr Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGTAA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGTATCACC 60

ATCACCTGCA AGGCCAGTCA GGATGTGACT ACTGCTGTAG CCTGGTATCA ACAAAAACCA 120

GGGCAATCTC CTAAACTTCT GATTACTGG GCATCCAQCC GGCACACTGG AGTCCCTGAT 180

CGCTTCACAG GCAGTGGATC TGGGACAGAT TATACTCTCA CCATCAGCAG TGTGCAGGCT 240
 GAAGACCTGG CACTTTATTA CTGTCAGCAA CATTATATCA CTCCGTGGAC GTTCGGTGGA 300
 GGGACCAAGC TGGAGATCT 319

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGCAGGAGT CAGGACCTGG CCTGGTGGCG CCCTCACAGA GCCTGTCCAT CACTTGCACT 60
 GTCTCTGGGT TTTCATTAA CAGCTATGGT GTACACTGGG TTCGCCAGCC TCCAGGAAAG 120
 GGTCTGGAGT GGCTGGGAGT CATTTGGGCT GGTGGAAGCA CAAATTATAA TTCGGCTCTC 180
 ATGTCCAGAC TGAACATCAA CAGAGACAAT TCCAAGAGCC AAATTTTCTT AAAAATGAAC 240
 AGTCTGCAAA CTGATGACAC AGCCATCTAC TACTGTGCCA GAGAGGGTTC TACGGTAGAT 300
 TCTATGGACT ACTGGGGCCA AGGGACCACG GTCACC 336

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACTGCAGCG GCCGCCATGG TGAAGCCATC ATTACC 36

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACTTGTGCG ACATTCTCTT TTGAAGTATT GC 32

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGATATCG TAATGACCCA GTCTCCA

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTAGATCTC CAGCTTGGTC CC

22

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala	Gly	Gly	Thr	Ser	Met	Ala	Arg	Cys	Thr	Gly	Cys	Ala	Gly	Ser	Ala
1				5					10					15	

Gly	Thr	Cys	Trp	Gly	Gly
			20		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGAGGAGACG GTGACCGTGG TCCCTTGGCC CC

32

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Phe Asn Val Glu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Glu Ile His Leu Tyr Gln
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Gln Asn Leu Val Ile Pro
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Cys Leu Glu His
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Asn Pro
1